

## SEQUENCE LISTING

**10/563896**  
**IAP20 Rec'd PCT/PTO 09 JAN 2006**

<110> JAPAN SCIENCE AND TECHNOLOGY AGENCY  
TAKEDA, Junji  
HORIE, Kyoji

<120> Method and sysytem for producing transgenic organisms using methylation

<130> KJ007PCT

<150> PCT/JP03/08681

<151> 2003-07-08

<160> 76

<170> PatentIn version 3.2

<210> 1

<211> 1455

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<213> Tanichthys albonubes

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<222> (1)..(1455)

<223> /note="Tcl-like transposon"

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<308> L48685

<309> 1996-05-31

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gac ctc cac aag tct ggt tca tcc ttg gga gca att tcc aaa cgc ctg 96
Asp Leu His Lys Ser Gly Ser Ser Leu Gly Ala Ile Ser Lys Arg Leu
20 25 30

aaa gta cca cgt tca tct gta caa aca ata gta cgc aag tat aaa cac 144
Lys Val Pro Arg Ser Ser Val Gln Thr Ile Val Arg Lys Tyr Lys His
35 40 45

cat ggg acc acg cag ccg tca tac cgc tca gga agg aga cgc gtt ctg 192
His Gly Thr Thr Gln Pro Ser Tyr Arg Ser Gly Arg Arg Arg Val Leu
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tct cct aga gat gaa cgt act ttg gtg cga aaa gtg caa atc aat ccc 240
Ser Pro Arg Asp Glu Arg Thr Leu Val Arg Lys Val Gln Ile Asn Pro
65 70 75 80

aga aca aca gca aag gac ctt gtg aag atg ctg gag gaa aca ggt aca 288
Arg Thr Thr Ala Lys Asp Leu Val Lys Met Leu Glu Glu Thr Gly Thr
85 90 95

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35 40 45

His Gly Thr Thr Gln Pro Ser Tyr Arg Ser Gly Arg Arg Arg Val Leu  
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Ser Pro Arg Asp Glu Arg Thr Leu Val Arg Lys Val Gln Ile Asn Pro  
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Arg Thr Thr Ala Lys Asp Leu Val Lys Met Leu Glu Glu Thr Gly Thr  
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Lys Val Ser Ile Ser Thr Val Lys Arg Val Leu Tyr Arg His Asn Leu  
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Lys Gly Arg Ser Ala Arg Lys Lys Pro Leu Leu Gln Asn Arg His Lys  
115 120 125

Lys Ala Arg Leu Arg Phe Ala Thr Ala His Gly Asp Lys Asp Arg Thr  
130 135 140

Phe Trp Arg Asn Val Leu Trp Ser Asp Glu Thr Lys Ile Glu Leu Phe  
145 150 155 160

Gly His Asn Asp His Arg Tyr Val Trp Arg Lys Lys Gly Glu Ala Cys  
165 170 175

Lys Pro Lys Asn Thr Ile Pro Thr Val Lys His Gly Gly Gly Ser Ile  
180 185 190

Met Leu Trp Gly Cys Phe Ala Ala Gly Gly Thr Gly Ala Leu His Lys  
195 200 205

Ile Asp Gly Ile Met Arg Lys Glu Asn Tyr Val Asp Ile Leu Lys Gln  
210 215 220

His Leu Lys Thr Ser Val Arg Lys Leu Lys Leu Gly Arg Lys Trp Val  
225 230 235 240

Phe Gln Met Asp Asn Asp Pro Lys His Thr Ser Lys Val Val Ala Lys  
245 250 255

Trp Leu Lys Asp Asn Lys Val Lys Val Leu Glu Trp Pro Ser Gln Ser  
260 265 270

Pro Asp Leu Asn Pro Ile Glu Asn Leu Trp Ala Glu Leu Lys Lys Arg  
275 280 285

Val Arg Ala Arg Arg Pro Thr Asn Leu Thr Gln Leu His Gln Leu Cys  
290 295 300

Gln Glu Glu Trp Ala Lys Ile His Pro Thr Tyr Cys Gly Lys Leu Val  
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Ile Leu Arg Ser Ala Arg Glu Asp Pro His Arg Thr Ala Thr Asp Ile	
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caa atg att ata agt tct cca aat gaa cct gta cca agt aaa cga act	630
Gln Met Ile Ile Ser Ser Pro Asn Glu Pro Val Pro Ser Lys Arg Thr	
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Val Arg Arg Arg Leu Gln Gln Ala Gly Leu His Gly Arg Lys Pro Val	
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Ala Lys Ala His Leu Arg Trp Gly Arg Gln Glu Trp Ala Lys His Ile	
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85 90 95 100	
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Leu Gln Asn Val Gly Arg Gly Phe Val Phe Gln Gln Asp Asn Asp Pro	
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His Leu Leu Asp Trp Pro Ser Gln Ser Pro Asp Leu Asn Pro Ile Glu	
200 205 210	
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His Leu Trp Glu Glu Leu Glu Arg Arg Leu Gly Gly Ile Arg Ala Ser	
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caa gct gtt att gat gca aac gga tac gcg aca aag tat taa            1344
Gln Ala Val Ile Asp Ala Asn Gly Tyr Ala Thr Lys Tyr
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<213> Caenorhabditis elegans

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Ser Lys Arg Thr Val Arg Arg Arg Leu Gln Gln Ala Gly Leu His Gly
35                40                45

Arg Lys Pro Val Lys Lys Pro Phe Ile Ser Lys Lys Asn Arg Met Ala
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Arg Val Ala Trp Ala Lys Ala His Leu Arg Trp Gly Arg Gln Glu Trp
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Ala Lys His Ile Trp Ser Asp Glu Ser Lys Phe Asn Leu Phe Gly Ser
85                90                95

Asp Gly Asn Ser Trp Val Arg Arg Pro Val Gly Ser Arg Tyr Ser Pro
100               105               110

Lys Tyr Gln Cys Pro Thr Val Lys His Gly Gly Gly Ser Val Met Val
115               120               125

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Ser Ile Met Asp Arg Phe Gln Tyr Glu Asn Ile Phe Glu Thr Thr Met

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Asn	Pro 210	Ile	Glu	His	Leu	Trp 215	Glu	Glu	Leu	Glu	Arg 220	Arg	Leu	Gly	Gly				
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Tyr.

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Tyr Ser Met Gln Lys Asn Phe Arg Leu Leu Gln Ile Ser Arg Ser Leu	
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Ala Thr Met Val Arg Gly Lys Pro Ile Ser Lys Glu Ile Arg Val Leu	
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Ile Arg Asp Tyr Phe Lys Ser Gly Lys Thr Leu Thr Glu Ile Ser Lys	
40 45 50	
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Gln Leu Asn Leu Pro Lys Ser Ser Val His Gly Val Ile Gln Ile Phe	
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Lys Lys Asn Gly Asn Ile Glu Asn Asn Ile Ala Asn Arg Gly Arg Thr	
70 75 80	
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Ser Ala Ile Thr Pro Arg Asp Lys Arg Gln Leu Ala Lys Ile Val Lys	
85 90 95	
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Ala Asp Arg Arg Gln Ser Leu Arg Asn Leu Ala Ser Lys Trp Ser Gln	
100 105 110 115	
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Gln Ile Phe Lys Lys Asn Gly Asn Ile Glu Asn Asn Ile Ala Asn Arg  
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Gly Arg Thr Ser Ala Ile Thr Pro Arg Asp Lys Arg Gln Leu Ala Lys  
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Ile Val Lys Ala Asp Arg Arg Gln Ser Leu Arg Asn Leu Ala Ser Lys  
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Trp Ser Gln Gln Leu Ala Lys Leu Ser Ser Glu Ser Gly Arg Asp Lys  
115 120 125

Leu Lys Ser Ile Gly Tyr Gly Phe Tyr Lys Ala Lys Glu Lys Pro Leu  
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Leu Thr Leu Arg Gln Lys Lys Lys Arg Leu Gln Trp Ala Arg Glu Arg  
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Met Ser Trp Thr Gln Arg Gln Trp Asp Thr Ile Ile Phe Ser Asp Glu  
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Ala Lys Phe Asp Val Ser Val Gly Asp Thr Arg Lys Arg Val Ile Arg  
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Lys Arg Ser Glu Thr Tyr His Lys Asp Cys Leu Lys Arg Thr Thr Lys  
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Phe Pro Ala Ser Thr Met Val Trp Gly Cys Met Ser Ala Lys Gly Leu  
210 215 220

Gly Lys Leu His Phe Ile Glu Gly Thr Val Asn Ala Glu Lys Tyr Ile  
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Asn Ile Leu Gln Asp Ser Leu Leu Pro Ser Ile Pro Lys Leu Leu Asp  
245 250 255

Cys Gly Glu Phe Thr Phe Gln Gln Asp Gly Ala Ser Ser His Thr Ala  
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Lys Arg Thr Lys Asn Trp Leu Gln Tyr Asn Gln Met Glu Val Leu Asp  
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Trp Pro Ser Asn Ser Pro Asp Leu Ser Pro Ile Glu Asn Ile Trp Trp  
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Leu Met Lys Asn Gln Leu Arg Asn Glu Pro Gln Arg Asn Ile Ser Asp  
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Leu Lys Ile Lys Leu Gln Glu Met Trp Asp Ser Ile Ser Gln Glu His  
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 Met Ser Gln  
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 Ala Thr Met Val Arg Gly Lys Pro Ile Ser Lys Glu Ile Arg Val Leu  
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ctt cat ttc att gaa ggg aca gtt aat gct gaa aaa tat att aat att Leu His Phe Ile Glu Gly Thr Val Asn Ala Glu Lys Tyr Ile Asn Ile 230 235 240	1132
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tca aat agt cca gat cta agc cca att gaa aat att tgg tgg cta atg	1324

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Lys	Asn	Gln	Leu	Arg	Asn	Glu	Pro	Gln	Arg	Asn	Ile	Ser	Asp	Leu	Lys		
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Lys	Gly	Asp	Val	Thr	Gln	Phe											
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Leu Thr Leu Arg Gln Lys Lys Lys Arg Leu Gln Trp Ala Arg Glu Arg  
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Met Ser Trp Thr Gln Arg Gln Trp Asp Thr Ile Ile Phe Ser Asp Glu  
 165 170 175

Ala Lys Phe Asp Val Ser Val Gly Asp Thr Arg Lys Arg Val Ile Arg  
 180 185 190

Lys Arg Ser Glu Thr Tyr His Lys Asp Cys Leu Lys Arg Thr Thr Lys  
 195 200 205

Phe Pro Ala Ser Thr Met Val Trp Gly Cys Met Ser Ala Lys Gly Leu  
 210 215 220

Gly Lys Leu His Phe Ile Glu Gly Thr Val Asn Ala Glu Lys Tyr Ile  
 225 230 235 240

Asn Ile Leu Gln Asp Ser Leu Leu Pro Ser Ile Pro Lys Leu Ser Asp  
 245 250 255

Cys Gly Glu Phe Thr Phe Gln Gln Asp Gly Ala Ser Ser His Thr Ala  
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Lys Arg Thr Lys Asn Trp Leu Gln Tyr Asn Gln Met Glu Val Leu Asp  
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Trp Pro Ser Asn Ser Pro Asp Leu Ser Pro Ile Glu Asn Ile Trp Trp  
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Leu Met Lys Asn Gln Leu Arg Asn Glu Pro Gln Arg Asn Ile Ser Asp  
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Leu Lys Ile Lys Leu Gln Glu Met Trp Asp Ser Ile Ser Gln Glu His  
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gagagcaact tttgttattg tgaagaaa atg gaa aaa gaa ttt cgt gtt ttg 352

Met Glu Lys Glu Phe Arg Val Leu  
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Ile Lys Tyr Cys Phe Leu Lys Gly Lys Asn Ala Val Glu Ala Lys Ser

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Trp Leu Asp Asn Glu Phe Pro Asp Ser Ala Pro Arg Lys Ser Ile Ile

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Ile Asp Trp Tyr Ala Lys Phe Lys Arg Gly Glu Met Ser Thr Glu Asp

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Gly Glu Arg Ser Gly Arg Pro Lys Glu Val Val Thr Asp Glu Asn Ile

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70

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Lys Lys Ile His Lys Met Ile Leu Asn Asp Arg Lys Met Lys Leu Ile

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Glu Ile Thr Lys Ala Leu Asn Ile Ser Lys Glu Arg Val Gly His Ile

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95

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Ile His Gln Tyr Leu Asp Met Arg Lys Leu Cys Ala Lys Trp Val Pro

105

110

115

120

cgc gaa ctc aca ttt gac caa aaa caa caa cgt gtt gat gat tct gag 736

Arg Glu Leu Thr Phe Asp Gln Lys Gln Gln Arg Val Asp Asp Ser Glu

125

130

135

cgg tgt ttg cag ctg tta act cgt aat aca ccc gag ttt ttc cgt cga 784

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140

145

150

tat gta aca atg gat gaa aca tgg ctc cat cac tac act cct gag ttc 832

Tyr Val Thr Met Asp Glu Thr Trp Leu His His Tyr Thr Pro Glu Phe

155

160

165

gat caa cag tcg gct gag tgg aca gcg acc ggt gaa ccg tct ccg aag 880

Asp Gln Gln Ser Ala Glu Trp Thr Ala Thr Gly Glu Pro Ser Pro Lys

170

175

180

cgt gga aag act caa aag tcc gct ggc aaa gta atg gcc tct gtt ttt 928  
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tgg aat gcg cat gga ata att ttt atc gat tat ctt gag aag gaa aaa 976  
 Trp Asn Ala His Gly Ile Ile Phe Ile Asp Tyr Leu Glu Lys Glu Lys  
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acc atc aac agt gac tat tat atg gcg tta ttg gag cgt ttg aag gtc 1024  
 Thr Ile Asn Ser Asp Tyr Tyr Met Ala Leu Leu Glu Arg Leu Lys Val  
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 Asp Leu Ala Pro Ser Glu Phe Phe Leu Phe Ser Asp Leu Lys Arg Leu  
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 Ala Gly Lys Lys Phe Gly Cys Asn Glu Glu Val Ile Ala Glu Thr Lys  
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 Ala Tyr Phe Glu Ala Lys Pro Lys Glu Tyr Tyr Gln Asn Gly Ile Lys  
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 Val Glu  
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Ser Ala Pro Arg Lys Ser Ile Ile Ile Asp Trp Tyr Ala Lys Phe Lys  
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Glu Val Val Thr Asp Glu Asn Ile Lys Lys Ile His Lys Met Ile Leu  
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Asn Asp Arg Lys Met Lys Leu Ile Glu Ile Thr Lys Ala Leu Asn Ile  
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Ser Lys Glu Arg Val Gly His Ile Ile His Gln Tyr Leu Asp Met Arg  
100 105 110

Lys Leu Cys Ala Lys Trp Val Pro Arg Glu Leu Thr Phe Asp Gln Lys  
115 120 125

Gln Gln Arg Val Asp Asp Ser Glu Arg Cys Leu Gln Leu Leu Thr Arg  
130 135 140

Asn Thr Pro Glu Phe Phe Arg Arg Tyr Val Thr Met Asp Glu Thr Trp  
145 150 155 160

Leu His His Tyr Thr Pro Glu Phe Asp Gln Gln Ser Ala Glu Trp Thr  
165 170 175

Ala Thr Gly Glu Pro Ser Pro Lys Arg Gly Lys Thr Gln Lys Ser Ala  
180 185 190

Gly Lys Val Met Ala Ser Val Phe Trp Asn Ala His Gly Ile Ile Phe  
195 200 205

Ile Asp Tyr Leu Glu Lys Glu Lys Thr Ile Asn Ser Asp Tyr Tyr Met  
210 215 220

Ala Leu Leu Glu Arg Leu Lys Val Glu Ile Ala Ala Lys Trp Pro His  
225 230 235 240

Met Lys Lys Lys Lys Val Leu Phe Asp Gln Asp Asn Ala Pro Cys His  
245 250 255

Lys Ser Val Arg Thr Met Ala Lys Ile His Glu Leu Gly Phe Glu Leu  
260 265 270

Leu Pro His Pro Leu Tyr Ser Pro Asp Leu Ala Pro Ser Glu Phe Phe  
275 280 285

Leu Phe Ser Asp Leu Lys Arg Leu Ala Gly Lys Lys Phe Gly Cys Asn  
290 295 300

Glu Glu Val Ile Ala Glu Thr Lys Ala Tyr Phe Glu Ala Lys Pro Lys  
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aagcaacttt tgttattgtg aaaaaa atg gaa aaa aag gaa ttt cgt gtt ttg 353  
Met Glu Lys Lys Glu Phe Arg Val Leu  
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Ile Lys Tyr Cys Phe Leu Lys Gly Lys Asn Thr Val Glu Ala Lys Thr  
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Trp Leu Asp Asn Glu Phe Pro Asp Ser Ala Pro Gly Lys Ser Thr Ile  
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att gat tgg tat gca aaa ttc aag cgt ggt gaa atg agc acg gag gac 497  
Ile Asp Trp Tyr Ala Lys Phe Lys Arg Gly Glu Met Ser Thr Glu Asp  
45 50 55  
ggg gaa cgc agt gga cgc ccg aaa gag gtg gtt acc gac gaa aac atc 545  
Gly Glu Arg Ser Gly Arg Pro Lys Glu Val Val Thr Asp Glu Asn Ile  
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Lys	Lys	Ile	His	Lys	Met	Ile	Leu	Asn	Asp	Arg	Lys	Met	Lys	Leu	Ile	
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Glu	Ile	Ala	Glu	Ala	Leu	Lys	Ile	Ser	Lys	Glu	Arg	Val	Gly	His	Ile	
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Ile	His	Gln	Tyr	Leu	Asp	Met	Arg	Lys	Leu	Cys	Ala	Lys	Trp	Val	Pro	
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Tyr	Val	Thr	Met	Asp	Glu	Thr	Trp	Leu	His	His	Tyr	Thr	Pro	Glu	Ser	
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Lys	Arg	Gln	Ser	Ala	Glu	Trp	Thr	Ala	Thr	Gly	Glu	Pro	Ser	Pro	Lys	
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cgt	gga	aag	act	caa	aag	tcc	gct	ggc	aaa	gta	atg	gcc	tct	gtt	ttt	929
Arg	Gly	Lys	Thr	Gln	Lys	Ser	Ala	Gly	Lys	Val	Met	Ala	Ser	Val	Phe	
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Phe	Asp	Ala	His	Gly	Ile	Ile	Phe	Ile	Asp	Tyr	Leu	Glu	Lys	Gly	Lys	
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Thr	Ile	Asn	Ser	Asp	Tyr	Tyr	Met	Ala	Leu	Leu	Glu	Arg	Leu	Lys	Val	
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gaa	atc	gcg	gca	aaa	cgg	ccc	cat	atg	aag	aag	aaa	aaa	gtg	ttg	ttc	1073
Glu	Ile	Ala	Ala	Lys	Arg	Pro	His	Met	Lys	Lys	Lys	Lys	Val	Leu	Phe	
	235					240					245					
cac	caa	gac	aac	gca	ccg	tgc	cac	aag	tca	ttg	aga	acg	atg	gca	aaa	1121
His	Gln	Asp	Asn	Ala	Pro	Cys	His	Lys	Ser	Leu	Arg	Thr	Met	Ala	Lys	
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Ile	His	Glu	Leu	Gly	Phe	Glu	Leu	Leu	Pro	His	Pro	Pro	Tyr	Ser	Pro	
				270					275					280		
gat	ctg	gcc	ccc	agc	gac	ttt	ttc	ttg	ttc	tca	gac	ctc	aaa	agg	atg	1217
Asp	Leu	Ala	Pro	Ser	Asp	Phe	Phe	Leu	Phe	Ser	Asp	Leu	Lys	Arg	Met	
			285					290					295			
ctc	gca	ggg	aaa	aaa	ttt	ggc	tgc	aat	gaa	gag	gtg	atc	gcc	gaa	act	1265
Leu	Ala	Gly	Lys	Lys	Phe	Gly	Cys	Asn	Glu	Glu	Val	Ile	Ala	Glu	Thr	
		300					305					310				
gag	gcc	tat	ttt	gag	gca	aaa	ccg	aag	gag	tac	tac	caa	aat	ggt	atc	1313
Glu	Ala	Tyr	Phe	Glu	Ala	Lys	Pro	Lys	Glu	Tyr	Tyr	Gln	Asn	Gly	Ile	
	315					320					325					
aaa	aaa	ttg	gaa	ggt	cgt	tat	aat	cgt	tgt	atc	gct	ctt	gaa	ggg	aac	1361

Lys Lys Leu Glu Gly Arg Tyr Asn Arg Cys Ile Ala Leu Glu Gly Asn  
330 335 340 345

tat gtt gaa taa taaaaacgaa ttttcacaaa aaaatgtgtt tttctttgtt 1413  
Tyr Val Glu

agaccgggga cttatcagcc aacctgttat cttgacgaaa aaatgaatgg tcgataaata 1473

atgtgatgtg atccttactg tgttcacttg actggacgaa accgttatga tcaatttgga 1533

tgccataaac 1543

<210> 19

<211> 348

<212> PRT

<213> Chrysoperla plorabunda

<400> 19

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1 5 10 15

Gly Lys Asn Thr Val Glu Ala Lys Thr Trp Leu Asp Asn Glu Phe Pro  
20 25 30

Asp Ser Ala Pro Gly Lys Ser Thr Ile Ile Asp Trp Tyr Ala Lys Phe  
35 40 45

Lys Arg Gly Glu Met Ser Thr Glu Asp Gly Glu Arg Ser Gly Arg Pro  
50 55 60

Lys Glu Val Val Thr Asp Glu Asn Ile Lys Lys Ile His Lys Met Ile  
65 70 75 80

Leu Asn Asp Arg Lys Met Lys Leu Ile Glu Ile Ala Glu Ala Leu Lys  
85 90 95

Ile Ser Lys Glu Arg Val Gly His Ile Ile His Gln Tyr Leu Asp Met  
100 105 110

Arg Lys Leu Cys Ala Lys Trp Val Pro Arg Glu Leu Thr Phe Asp Gln  
115 120 125

Lys Gln Gln Arg Val Asp Asp Ser Glu Arg Cys Leu Gln Leu Leu Thr  
130 135 140

Arg Asn Thr Pro Glu Phe Leu Arg Arg Tyr Val Thr Met Asp Glu Thr  
145 150 155 160

Trp Leu His His Tyr Thr Pro Glu Ser Lys Arg Gln Ser Ala Glu Trp  
165 170 175

Thr Ala Thr Gly Glu Pro Ser Pro Lys Arg Gly Lys Thr Gln Lys Ser

180

185

190

Ala Gly Lys Val Met Ala Ser Val Phe Phe Asp Ala His Gly Ile Ile  
195 200 205

Phe Ile Asp Tyr Leu Glu Lys Gly Lys Thr Ile Asn Ser Asp Tyr Tyr  
210 215 220

Met Ala Leu Leu Glu Arg Leu Lys Val Glu Ile Ala Ala Lys Arg Pro  
225 230 235 240

His Met Lys Lys Lys Lys Val Leu Phe His Gln Asp Asn Ala Pro Cys  
245 250 255

His Lys Ser Leu Arg Thr Met Ala Lys Ile His Glu Leu Gly Phe Glu  
260 265 270

Leu Leu Pro His Pro Pro Tyr Ser Pro Asp Leu Ala Pro Ser Asp Phe  
275 280 285

Phe Leu Phe Ser Asp Leu Lys Arg Met Leu Ala Gly Lys Lys Phe Gly  
290 295 300

Cys Asn Glu Glu Val Ile Ala Glu Thr Glu Ala Tyr Phe Glu Ala Lys  
305 310 315 320

Pro Lys Glu Tyr Tyr Gln Asn Gly Ile Lys Lys Leu Glu Gly Arg Tyr  
325 330 335

Asn Arg Cys Ile Ala Leu Glu Gly Asn Tyr Val Glu  
340 345

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<220>  
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ccaacttatt gtgggaagct tgtggaaggc tactcgaaat gtttgacca agttaaacia 120  
tttaaaggca atgctaccaa atactaattg agtgtatgtt aacttctgac ccaactgggaa 180  
tgtgatgaaa gaaataaaaag ctgaaatgaa tcattctctc tactattatt ctgatatttc 240  
acattcttaa aataaagtgg tgatcctaac tgaccttaag acaggaatc ttactcgga 300  
ttaaatgtca ggaattgtga aaaagtgagt ttaaatgtat ttggctaagg tgtatgtaaa 360  
cttccgactt caactgta 378

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 <211> 354  
 <212> DNA  
 <213> Artificial

<220>  
 <223> IR/DR-L

<400> 21  
 ccttgaaata catccacagg tacacctcca attgactcaa atgatgtcaa ttagtctatc 60  
 agaagcttct aaagccatga catcattttc tggaattttc caagctgttt aaaggcacag 120  
 tcaacttagt gtatgtaaac ttctgacca ctggaattgt gatacagtga attataagtg 180  
 aaataatctg tctgtaaaca attgttgga aaatgacttg tgtcatgcac aaagtagatg 240  
 tcctaactga cttgccaaaa ctattgtttg ttaacaagaa atttgtggag tagttgaaaa 300  
 acgagtttta atgactccaa ctttaagtga tgtaaacttc cgacttcaac tgta 354

<210> 22  
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<220>  
 <223> 5' outer repeat

<400> 22  
 gttcaagtcg gaagtttaca tacacttag 29

<210> 23  
 <211> 30  
 <212> DNA  
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<220>  
 <223> 5' inner repeat

<400> 23  
 cagtgggtca gaagtttaca tacactaagg 30

<210> 24  
 <211> 31  
 <212> DNA  
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<220>  
 <223> 3' inner repeat

<400> 24  
 cagtgggtca gaagttaaca tacactcaat t 31

<210> 25  
 <211> 30  
 <212> DNA  
 <213> Artificial

<220>  
 <223> 3' outer repeat



<400> 25  
agttgaatcg gaagttttaca tacaccttag 30

<210> 26  
<211> 30  
<212> DNA  
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<220>  
<223> preferred consensus direct repeat

<400> 26  
caktgrgtcr gaagttttaca tacacttaag 30

<210> 27  
<211> 26  
<212> DNA  
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<220>  
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<400> 27  
gttgaagtcg gaagttttaca cttagg 26

<210> 28  
<211> 31  
<212> DNA  
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<220>  
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<400> 28  
ccagtgggtc aggaagttta catacactaa g 31

<210> 29  
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<212> DNA  
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<220>  
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<400> 29  
catgccatgg gaaaatcaaa agaaatc 27

<210> 30  
<211> 26  
<212> DNA  
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<220>  
<223> reverse sequence used for PCR amplication from pCMV-SB

<400> 30  
ccgctcgagc agtggcttct tccttg 26

<210> 31

<211> 25  
 <212> DNA  
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<220>  
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<400> 31  
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<210> 32  
 <211> 25  
 <212> DNA  
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<220>  
 <223> primer EGFP-1L

<400> 32  
 cttgatgccg ttcttctgct tgcg 25

<210> 33  
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<220>  
 <223> primer HYG-1U

<400> 33  
 cgggcgtata tgctcccat tggctcttgac 30

<210> 34  
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<220>  
 <223> primer TK-1L

<400> 34  
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<210> 35  
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<220>  
 <223> primer M13F

<400> 35  
 acgacgttgt aaaacgacgg ccagt 25

<210> 36  
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<400> 36  
gcacgcgcat gggtcacgac gagatcctc 29

<210> 37  
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<400> 37  
aagtgagttt aaatgtattt ggctaaggtg 30

<210> 38  
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<220>  
<223> TgTP-2L

<400> 38  
acacaggaaa cagctatgac catgattacg 30

<210> 39  
<211> 25  
<212> DNA  
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<220>  
<223> primer neo-U1

<400> 39  
gggtggagag gctattcggc tatga 25

<210> 40  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<223> primer neo-L1

<400> 40  
tggatacttt ctcggcagga gcaag 25

<210> 41  
<211> 23  
<212> DNA  
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<220>  
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<220>  
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<400> 41  
cggccgctct agcgggtaccc tac

23

<210> 42  
<211> 22  
<212> DNA  
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<220>  
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<220>  
<221> misc\_feature  
<222> (1)..(1)  
<223> connected to LCRed640

<400> 42  
gtaggggatc gacctcgagg gg

22

<210> 43  
<211> 25  
<212> DNA  
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<220>  
<223> probe

<220>  
<221> misc\_feature  
<222> (1)..(1)  
<223> connected to FITC

<400> 43  
gctgtgctcg acgttgctac tgaag

25

<210> 44  
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<212> DNA  
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<220>  
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<220>  
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<223> connected to LCRed640

<400> 44  
gggaaggac tggctgctat tggg

24

<210> 45  
<211> 20  
<212> DNA  
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<220>  
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<400> 45  
gttgggtcgt ttgttcggat 20

<210> 46  
<211> 20  
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<220>  
<223> PCR primer

<400> 46  
cgcgcaatta accctcacta 20

<210> 47  
<211> 20  
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<220>  
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<400> 47  
aatgaactgc aggacgaggc 20

<210> 48  
<211> 20  
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<220>  
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<400> 48  
atggatactt tctcggcagg 20

<210> 49  
<211> 30  
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<220>  
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<400> 49  
ttcctaaaaga agtagagtgg agaaccagtg 30

<210> 50  
<211> 23  
<212> DNA  
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<220>  
<223> primer PGK2

<400> 50  
aggccacttg tgtagcgcca agt 23

<210> 51

<211> 30  
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<220>  
 <223> primer LCB2XL1

<400> 51  
 ccaaccaa acatttaaca tattctaggt

30

<210> 52  
 <211> 26  
 <212> DNA  
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<220>  
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<400> 52  
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26

<210> 53  
 <211> 30  
 <212> DNA  
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<220>  
 <223> forward primer for amlication of SB transposase gene

<400> 53  
 aatagaactg tttggccata atgaccatcg

30

<210> 54  
 <211> 25  
 <212> DNA  
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<220>  
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<400> 54  
 atccacataa ttttccttcc tcatg

25

<210> 55  
 <211> 30  
 <212> DNA  
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<220>  
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<400> 55  
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30

<210> 56  
 <211> 30  
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<220>  
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<400> 56  
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30

<210> 57  
<211> 30  
<212> DNA  
<213> Artificial

<220>  
<223> primer beta geo

<400> 57  
tgccagtttg aggggacgac gacagtatcg

30

<210> 58  
<211> 30  
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<220>  
<223> MS specific primer

<400> 58  
tggagtgagc tagaatcaga aagatgacac

30

<210> 59  
<211> 30  
<212> DNA  
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<220>  
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<400> 59  
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30

<210> 60  
<211> 30  
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<400> 60  
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30

<210> 61  
<211> 30  
<212> DNA  
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<220>  
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<400> 61  
gatatgaaga gctgtcagtt tgtagcagtc

30

<210> 62

<211> 34  
<212> DNA  
<213> Artificial

<220>  
<223> Unmet-U

<400> 62  
tacagttgaa gtcggaagtt tacatacact taag

34

<210> 63  
<211> 34  
<212> DNA  
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<220>  
<223> Unmet-L

<400> 63  
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34

<210> 64  
<211> 34  
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<220>  
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<400> 64  
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34

<210> 65  
<211> 34  
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<220>  
<223> Met-L

<220>  
<221> misc\_feature  
<222> (21)..(21)  
<223> N is 5-methyl cytosine

<400> 65  
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34

<210> 66  
<211> 25  
<212> DNA  
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<220>  
<223> forward primer for amylase 2.1 gene



<400> 66  
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25

<210> 67  
<211> 25  
<212> DNA  
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<220>  
<223> reverse primer for amylase 2.1 gene

<400> 67  
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25

<210> 68  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 68  
tgcgaggata agaacagaca ctac

24

<210> 69  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 69  
acagactcag aagcaaactg aaga

24

<210> 70  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<223> forward primer sequence for IR/DR-L

<400> 70  
gcacgggtgt tgggtcgttt gttc

24

<210> 71  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> reverse primer sequence for IR/DR-L

<400> 71  
cttctaaagc catgacatca ttttctg

27

<210> 72

<211> 28  
<212> DNA  
<213> Artificial

<220>  
<223> forward primer sequence for IR/DR-R

<400> 72  
gaaggctact cgaaatgttt gacccaag 28

<210> 73  
<211> 24  
<212> DNA  
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<220>  
<223> EGFP-1U primer

<400> 73  
cacgctggcg accagcctga ccta 24

<210> 74  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<223> EGFP-1L primer

<400> 74  
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<210> 75  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<223> SB-2U primer

<400> 75  
tcctagagat gaacgtactt tggc 24

<210> 76  
<211> 25  
<212> DNA  
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<220>  
<223> SB-1L primer

<400> 76  
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